

Table S1. Percentage of NKp44 reporter cells expressing GFP after individual retesting of the top 30 candidate protein hits from the initial secretome library screen. Related to Figure 1.

Protein	Hit #	Dilution						
		1/10	1/20	1/40	1/80	1/160	1/320	1/640
PDGF-D	1	49.2	31.5	23.6	13.2	9.59	6.06	3.04
CCL2	2	0.834	0.537	0.795	0.619	0.251	0.515	0.421
IL-17	3	0.683	0.229	0.189	0.618	0.389	0.225	0.175
BOLA3	4	0.912	0.497	0.265	0.235	0.06	0.342	0.235
OBP2B	5	0.651	1.18	0.412	0.338	0.391	0.307	0.186
WFDC5	6	0.584	0.423	0.352	0.604	0.494	0.442	0.291
CCL2	7	0.965	0.396	0.296	0.534	0.798	0.545	0.499
SLURP1	8	0.516	0.213	0.649	0.284	0.293	0.365	0.571
OBP2A	9	0.684	0.219	0.792	0.855	1.09	0.585	0.63
C1QTNF1	10	0.551	0.506	0.382	0.58	0.338	0.456	0.4
PLA2G1B	11	0.905	0.568	0.613	0.558	0.48	0.365	0.443
FAM171A1	12	2.01	1.18	1.22	0.368	0.89	0.649	0.868
INSL4	13	0.349	0.751	0.225	0.291	0.525	0.786	0.637
IL-10	14	2.13	1.41	0.446	0.729	0.765	0.877	0.814
SPACA3	15	0.776	0.543	0.595	0.509	0.844	0.301	0.489
ERP29	16	1.63	5.06	0.986	1.42	0.846	0.707	0.489
IFNA6	17	0.945	1.22	0.76	0.637	0.696	0.148	0.154
SPINK7	18	0.386	0.675	0.533	0.497	0.209	0.344	0.426
ARHGAP36	19	0.447	0.365	0.482	0.426	0.348	0.41	0.341
IFNA14	20	0.451	0.661	0.574	0.425	0.896	0.318	0.398
TF	21	0.718	0.685	0.336	0.388	0.641	0.344	0.383
RIC3	22	0.677	0.369	0.339	0.396	0.551	0.353	0.401
IL-4	23	1.92	1.83	1.09	0.655	0.815	0.512	0.439
CCL1	24	0.314	0.421	0.613	0.621	0.637	0.872	0.503
CPO	25	0.634	0.56	0.684	0.468	0.786	0.663	0.752
CST3	26	0.806	1.06	0.677	0.579	0.688	0.347	0.452
TNF- α	27	0.869	0.592	0.345	0.405	0.465	0.588	0.458
KLK7	28	0.958	1.14	0.573	0.843	0.487	0.468	0.575
C18orf56	29	0.268	0.284	1.02	0.931	0.468	0.575	0.604
ANGPTL1	30	0.256	0.719	0.532	0.711	0.758	0.603	0.434

Table S2. Linear coefficients underlying the canonical cytokine covariate for *NCR2* and the Pearson correlation coefficient results between individual cytokine genes and *NCR2*. Related to Figure 5.

Cytokine Gene	Coefficients used to construct canonical cytokine variate for <i>NCR2</i> using cytokine genes	Correlation between cytokine genes with canonical cytokine variate for <i>NCR2</i>
<i>CCL1</i>	0.372005	0.718842
<i>LTA</i>	0.191506	0.563069
<i>XCL1</i>	0.357679	0.70123
<i>CCL4</i>	-0.24997	-0.10706
<i>CSF2</i>	0.344527	0.647489
<i>IFNG</i>	0.146162	0.489111
<i>TNF</i>	0.163326	0.322124

Table S3. Linear coefficients underlying the canonical cell cycle covariate for *NCR2* and the Pearson correlation coefficient results between individual cell cycle genes and *NCR2*. Related to Figure 5.

Cell Cycle Gene	Coefficients used to construct canonical cell cycle variate for <i>NCR2</i> using cell cycle genes	Pearson correlation coefficients between cell cycle genes with canonical cell cycle variate for <i>NCR2</i>
<i>CDKN3</i>	-0.05769	-0.24054
<i>CCNB1</i>	0.061921	-0.30666
<i>CLSPN</i>	0.245624	0.369497
<i>CDC6</i>	-0.17238	-0.37589
<i>E2F2</i>	0.326543	0.611553
<i>CDC20</i>	0.293925	-0.25356
<i>NUSAP1</i>	0.531738	-0.31351
<i>BUB1B</i>	-0.12186	-0.3768
<i>KIFC1</i>	0.419413	-0.1862
<i>NCAPG</i>	0.069759	-0.28995
<i>ASPM</i>	0.244336	-0.35133
<i>CENPF</i>	-0.35454	-0.36108
<i>CCNA2</i>	0.096712	-0.27346
<i>CEP55</i>	-0.39911	-0.40452
<i>PRC1</i>	-0.86648	-0.49728
<i>ZWINT</i>	0.117411	-0.38032
<i>ERCC6L</i>	0.325993	-0.23011
<i>AURKA</i>	0.317172	-0.25134
<i>CDCA3</i>	-0.08287	-0.25541
<i>PLK1</i>	0.168593	-0.24751
<i>OIP5</i>	-0.08881	-0.32462
<i>CENPE</i>	-0.15391	-0.40178
<i>E2F1</i>	0.203567	-0.14298
<i>MAD2L1</i>	0.020655	-0.36918
<i>FBXO5</i>	-0.67962	-0.55774
<i>CCNF</i>	-0.27297	-0.20532
<i>NUP37</i>	-0.19051	-0.34827